

C.

Axis number	Polarity
10	1
11	0.4
12	1
13	0.4
14	0.8
15	0.2
16	0.8
17	0.8
18	0.6
19	0.8
20	0.8
21	0.8
22	0.8
Average	0.708

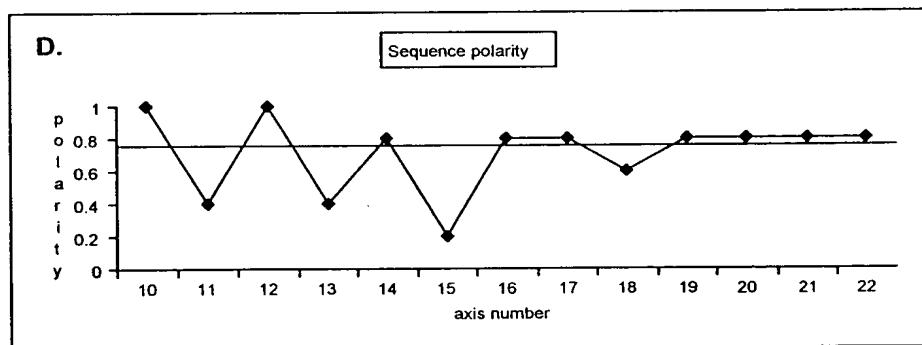
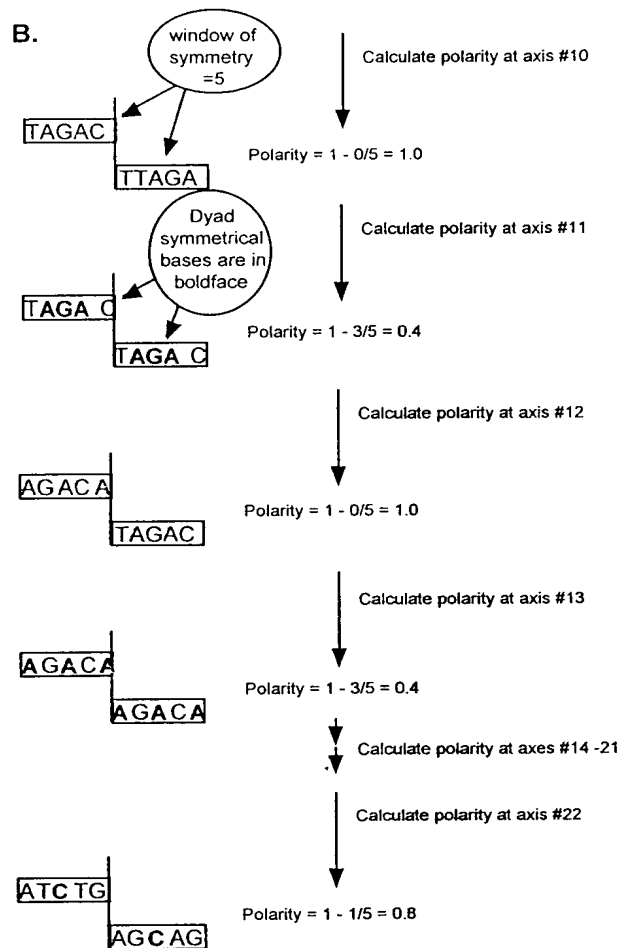


FIGURE 1

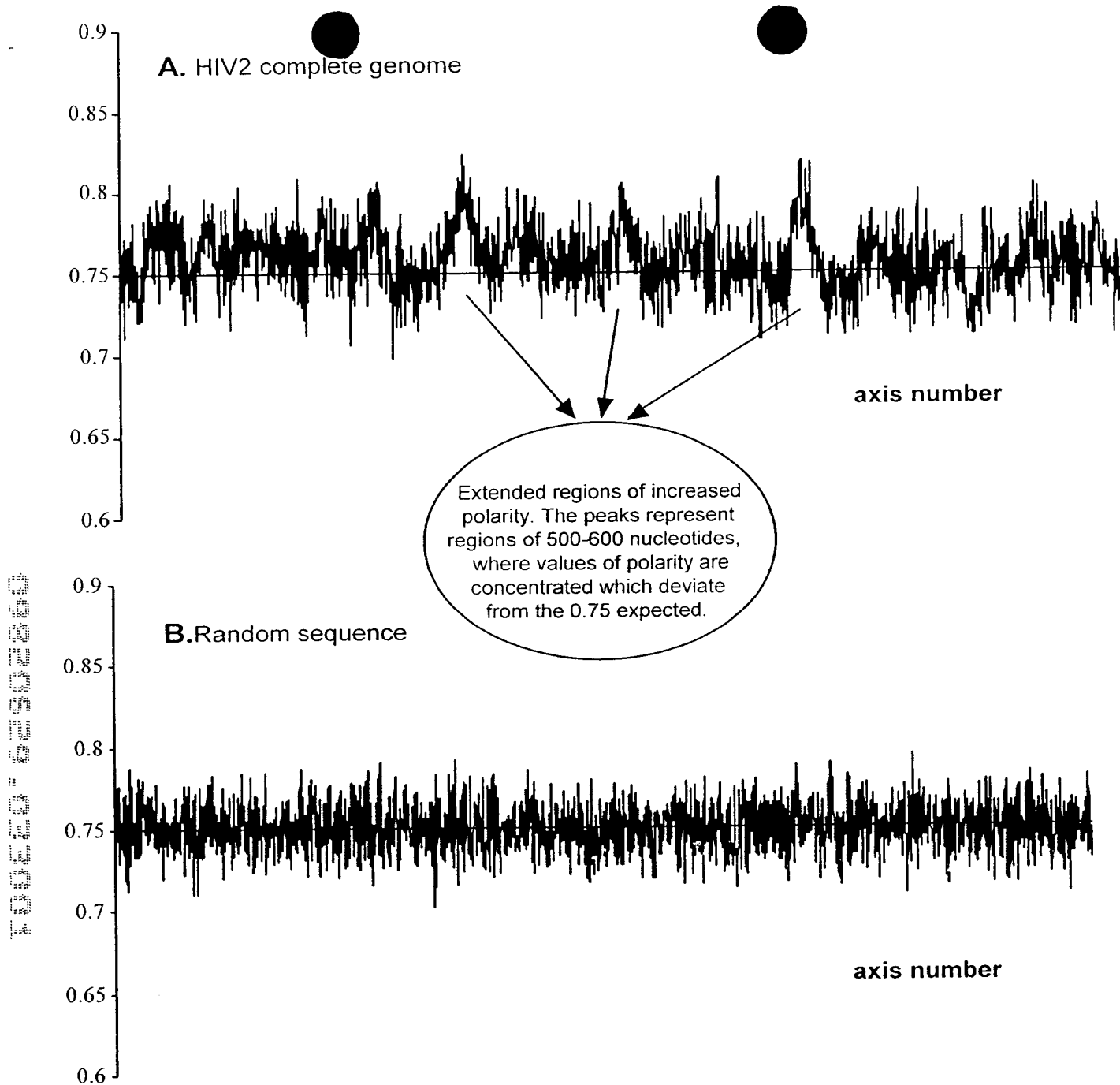
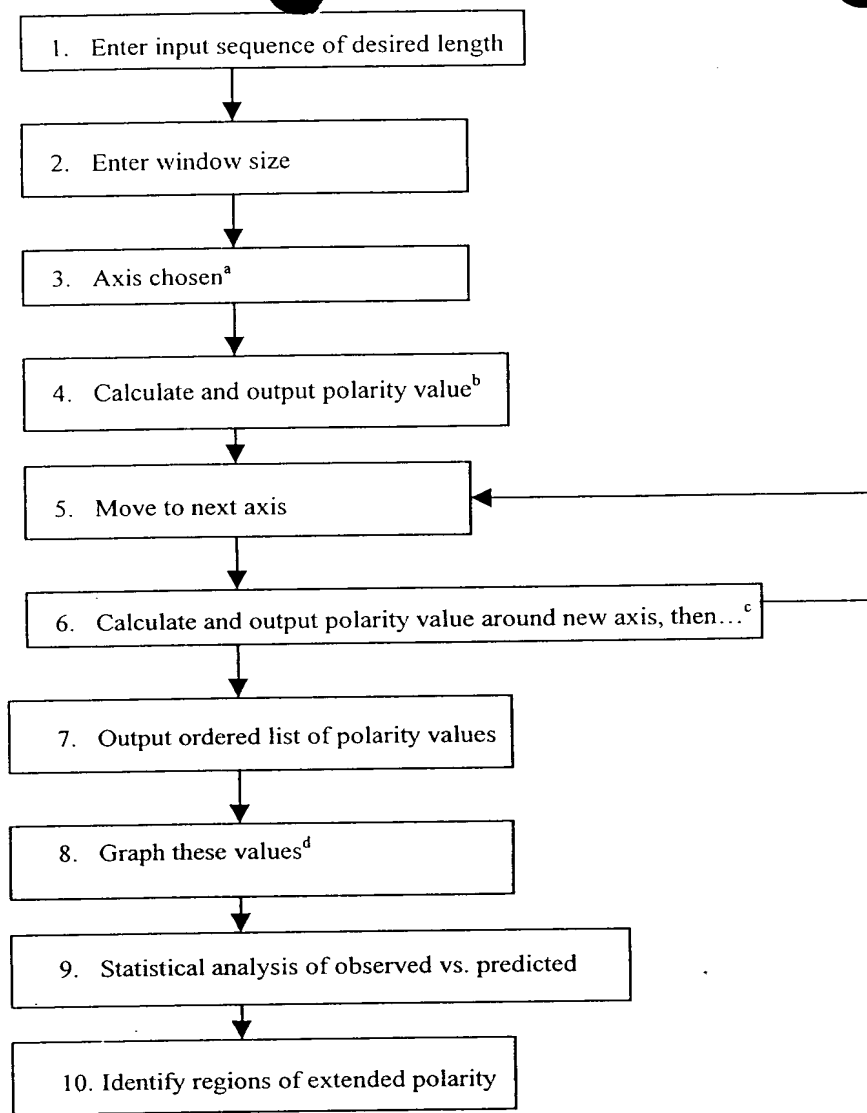


FIGURE 2



<sup>a</sup> Starting at position =  $(2 * \text{window of symmetry})$

<sup>b</sup>  $[1 - (S/W)]$

<sup>c</sup> Up to and including axis position =  $[2 * \text{length} - (2 * \text{window size})]$

<sup>d</sup> Can use a moving average of values (with number of values averaged and increment of moving being variable) to smooth curve

FIGURE 3

The algorithm was implemented in PERL programming language.  
 PERL variable-names and function-names are in boldface.

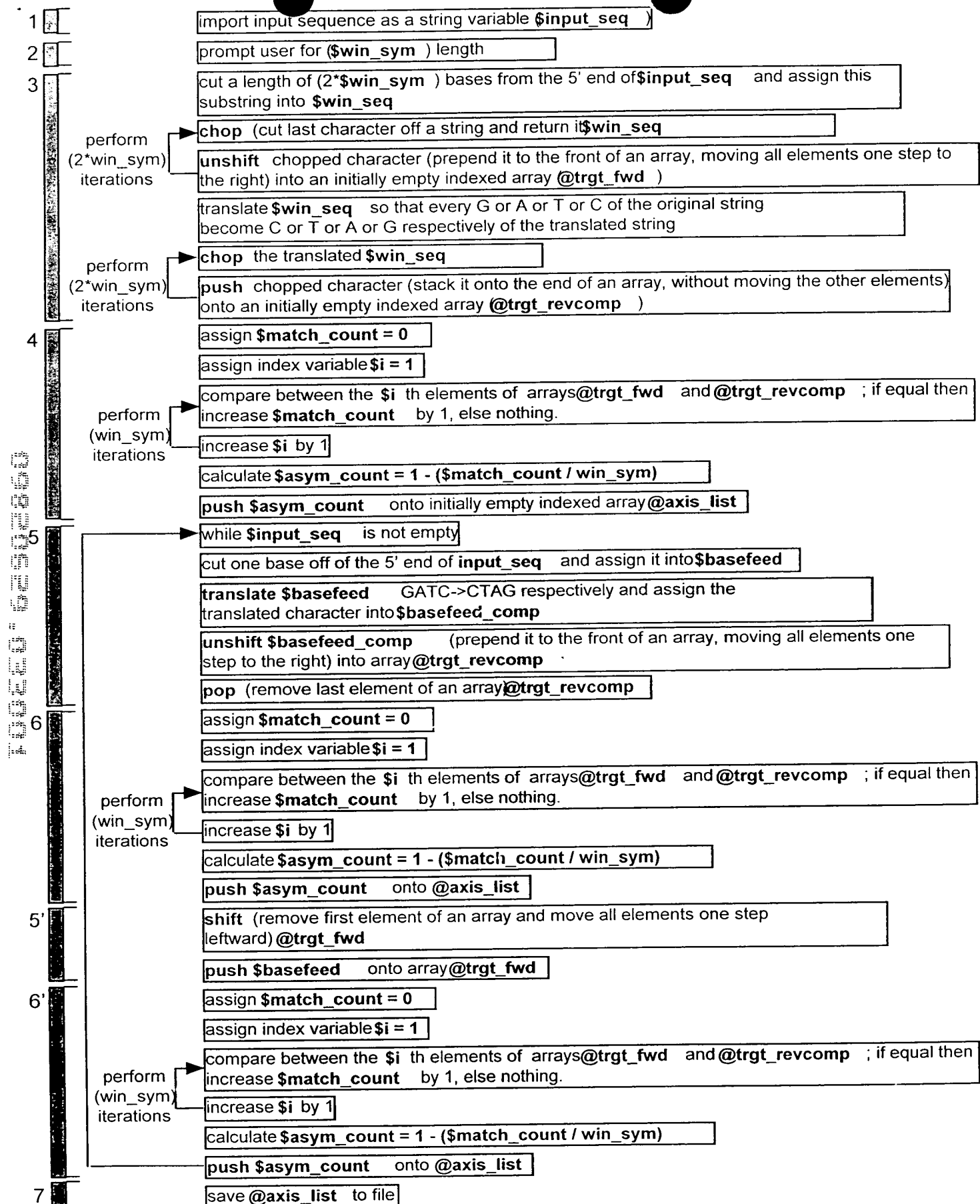
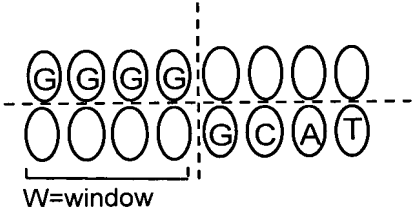


FIGURE 4

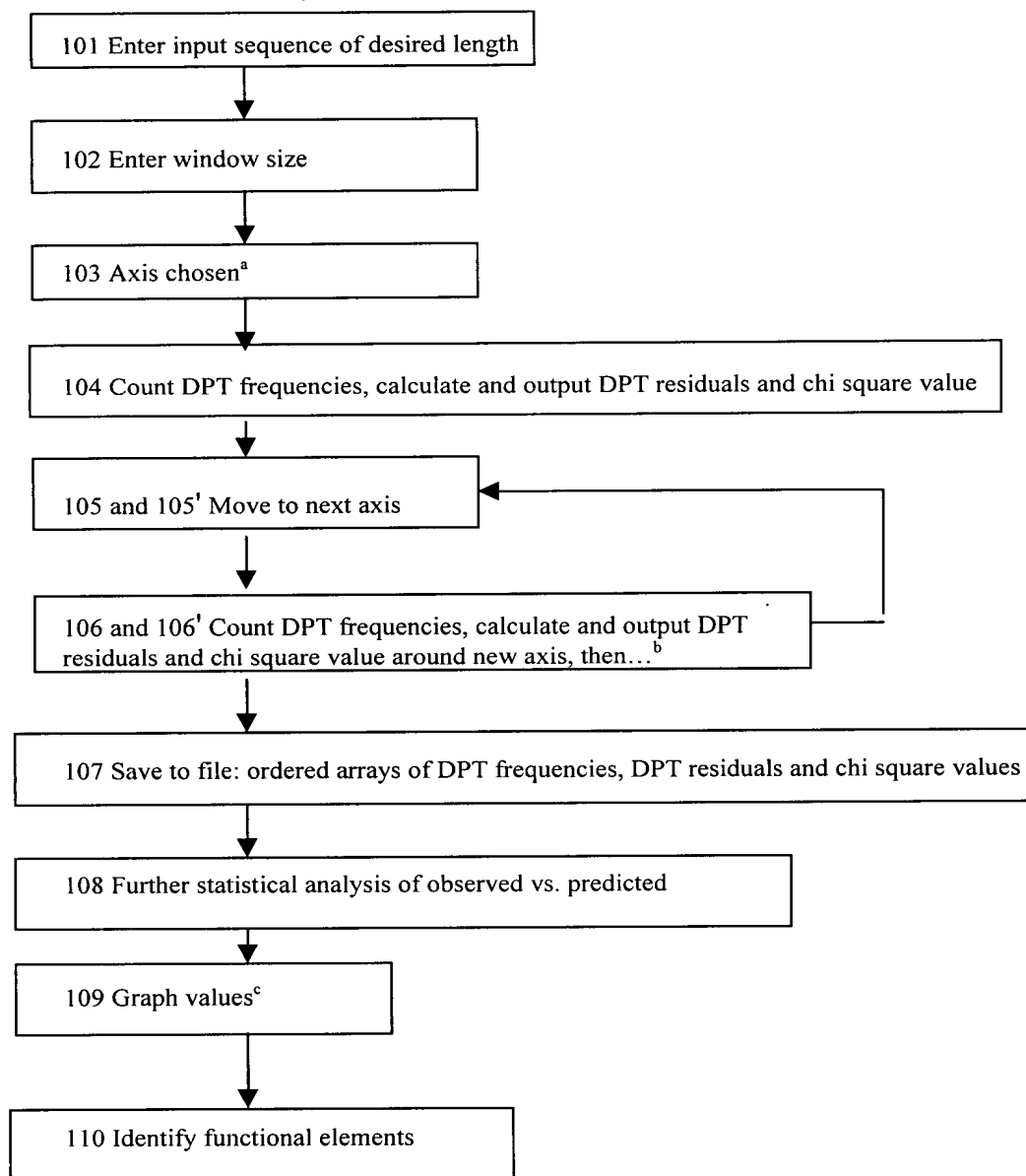
self dyad	self mirror	Purine pyrimidine dyad	Purine pyrimidine mirror
i=1: <sup>G</sup> --G	i=5: <sup>G</sup> --C	i=9: <sup>G</sup> --A	i=13: <sup>G</sup> --T
i=2: <sup>A</sup> --A	i=6: <sup>A</sup> --T	i=10: <sup>A</sup> --G	i=14: <sup>A</sup> --C
i=3: <sup>T</sup> --T	i=7: <sup>T</sup> --A	i=11: <sup>T</sup> --C	i=15: <sup>T</sup> --G
i=4: <sup>C</sup> --C	i=8: <sup>C</sup> --G	i=12: <sup>C</sup> --T	i=16: <sup>C</sup> --A

↑  
Figure 5A

Figure 5B  
↓



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<sup>a</sup> Starting at axis position =  $(2 * \text{window size})$

<sup>b</sup> Up to and including axis position =  $[2 * \text{length} - (2 * \text{window size})]$

<sup>c</sup> Values include DPT frequencies, statistical measures including residuals and  $\chi^2$

FIGURE 6

The algorithm was implemented in PERL programming language.  
PERL variable names and function names are in boldface.

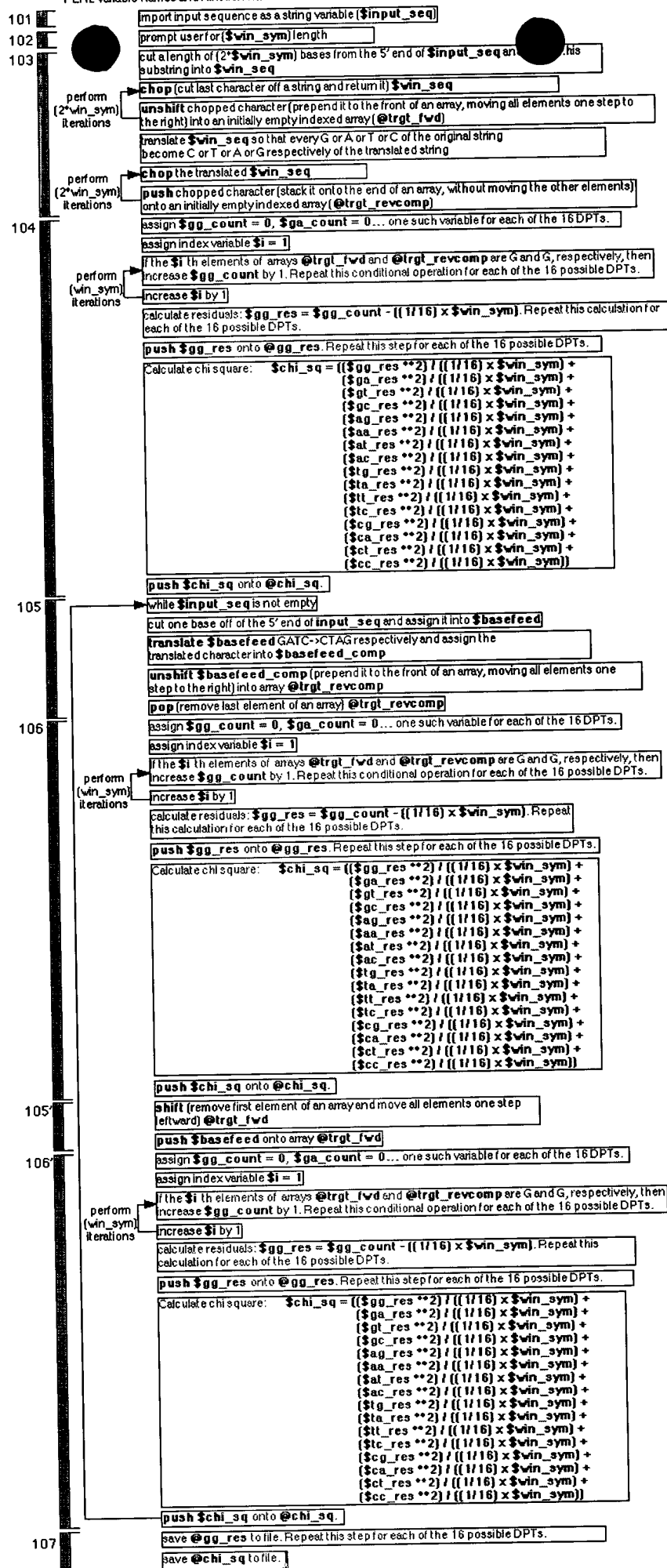


FIGURE 7



FIGURE 8



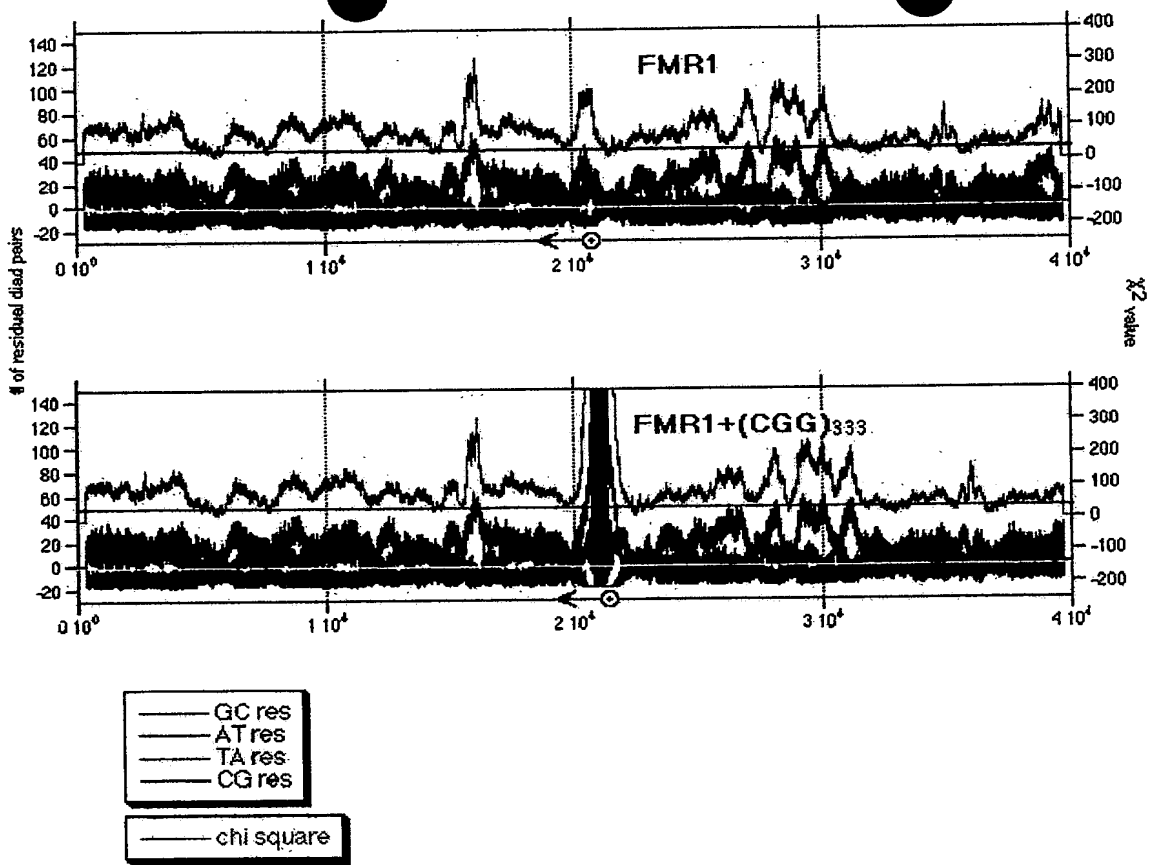


FIGURE 9

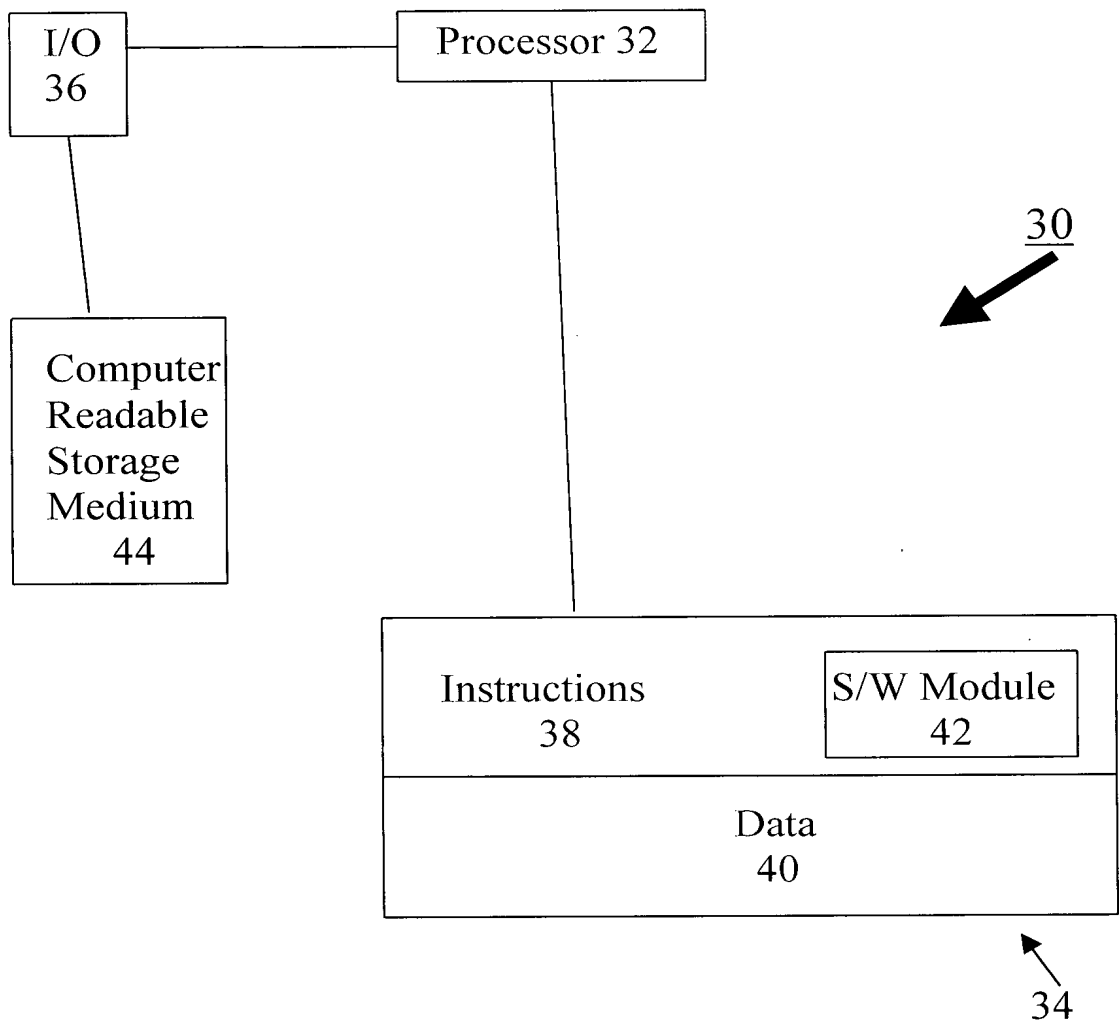


FIGURE 10